



Attorney's Docket No.: 10448-081001 / MPI2000-336P1R

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Rory A. J. Curtis Art Unit : Unknown
Serial No. : 09/934,323 Examiner : Unknown
Filed : August 21, 2001
Title : 33410, A NOVEL HUMAN CARBOXYLESTERASE FAMILY MEMBER AND
USES THEREOF

BOX MISSING PARTS

Commissioner for Patents
Washington, D.C. 20231

AMENDMENT AND RESPONSE TO NOTICE TO FILE MISSING PARTS

In response to the Notice to File Missing Parts of Application filed under 37 CFR §1.53(b) dated September 13, 2001 (copy enclosed), Applicant, as a large entity, submits herewith the following:

- Check in payment of \$130 surcharge for filing the declaration on a date later than the filing date of the application;
- Executed Combined Declaration and Power of Attorney in compliance with 37 CFR §1.63 (2 pages);
- Substitute Drawings (4 sheets);
- a Sequence Listing in computer readable form as required by 37 CFR §1.824, an initial Sequence Listing (14 pages) as required under 37 CFR §1.823(a) and a statement under 37 CFR §1.821(f); and
- a Petition for One Month Extension of Time, along with a check for \$110 for the required extension fee.

Applicant respectfully requests entry of the paper copy and computer readable copy of the Sequence Listing filed herewith for the instant application. Furthermore, applicant requests entry of the following amendments.

CERTIFICATE OF MAILING BY FIRST CLASS MAIL

I hereby certify under 37 CFR §1.8(a) that this correspondence is being deposited with the United States Postal Service as first class mail with sufficient postage on the date indicated below and is addressed to the Commissioner for Patents, Washington, D.C. 20231.

December 13, 2001

Date of Deposit

Signature

Jennifer Hess Carleton

Typed or Printed Name of Person Signing Certificate

In the specification:

Insert the paper copy of the Sequence Listing filed herewith following the Oath/Declaration.

Replace the paragraph beginning at page 10, line 29, with the following rewritten paragraph:

--*Figure 3* depicts alignment of the rat neuroligin-2 amino acid sequence and the human 33410 (SEQ ID NO:2) amino acid sequences. The location of the transmembrane domain in the rat neuroligin-2 (SEQ ID NO:5) and 33410 amino acid sequences is indicated as "TM1".--

Replace the paragraph beginning at page 10, line 32, with the following rewritten paragraph:

--*Figure 4* depicts alignment of the partial human KIAA1366 (Genbank Accession Number AB037787; SEQ ID NO:6) and the human 33410 amino acid sequences (SEQ ID NO:2).--

Replace the paragraph beginning at page 12, line 27, with the following rewritten paragraph:

--Carboxylesterase family members are characterized by a catalytic triad of amino acids: a serine, a glutamate or aspartate and a histidine. The sequence around the active site serine is well conserved and can be used as a signature pattern. A second signature pattern is located in the N-terminal section and contains a cysteine involved in disulfide bond formation. Typical consensus patterns of carboxylesterases are F-[GR]-G-x(4)-[LIVM]-x-[LIV]-x-G-x-S-[STAG]-G (SEQ ID NO:7) (where S is the active site residue) and [ED]-D-C-L-[YT]-[LIV]-[DNS]-[LIV]-[LIVFYW]-x-[PQR] (where C is involved in a disulfide bond). 33410 proteins have a similar pattern starting at about amino acid 252 to 267 of SEQ ID NO:2 as follows:

FGGDPERITIFGSGAG.--

Replace the paragraph beginning at page 14, line 4, with the following rewritten paragraph:

--As used herein, the term "carboxylesterase domain" refers to a protein domain which includes a carboxylesterase type B signature 2 domain. Preferably, the carboxylesterase type B signature 2 domain is about 5 to 20 amino acids, more preferably 8-15, most preferably 11 amino acids and includes the sequence [EDX(0,1)CLYX] (SEQ ID NO:8). Most preferably, the carboxylesterase type B signature 2 domain has the amino acid sequence: EDCLYNINYVP located at about amino acids 139 to 149 of SEQ ID NO:2. Preferably, the carboxylesterase domain has an amino acid sequence of about 450 to about 650 amino acid residues and having a bit score for the alignment of the sequence to the carboxylesterase domain (HMM) of at least 100. Preferably, a carboxylesterase domain includes at least about 450 to about 600 amino acids, more preferably about 500 to about 575 amino acid residues, about 550 to 570, or about 559 amino acids and has a bit score for the alignment of the sequence to the carboxylesterase domain (HMM) of at least 200, preferably 300, more preferably 400 or greater. The carboxylesterase domain (HMM) has been assigned the PFAM Accession (PF00135) (<http://genome.wustl.edu/Pfam/html>). An alignment of the carboxylesterase domain (from about amino acids 42 to about 601 of SEQ ID NO:2) of human 33410 with a consensus amino acid sequence derived from a hidden Markov model (PFAM) is depicted in Figure 3.--

In the drawings:

Substitute the enclosed 4 sheets of formal drawings for the informal drawings as filed.

Applicant : 'Rory A. J. Curtis
Serial No. : 09/934,323
Filed : August 21, 2001
Page : 4'

Attorney's Docket No.: 10448-081001 / MPI2000-
336P1R

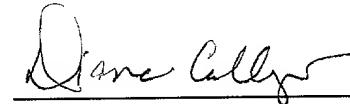
REMARKS

Applicant hereby submits that the enclosures fulfill the requirements under 37 C.F.R. §1.821-1.825. The amendments in the specification merely insert the paper copy of the Sequence Listing and sequence identifiers in the specification. No new matter has been added.

Attached hereto is a marked-up version of the changes made to the specification by the current amendment.

Please apply any charges or credits to Deposit Account No. 06-1050, referencing matter number 10448-081001.

Respectfully submitted,



Diana M. Collazo
Reg. No. 46,635

Fish & Richardson P.C.
225 Franklin Street
Boston, Massachusetts 02110-2804
Telephone: (617) 542-5070
Facsimile: (617) 542-8906

Version With Markings to Show Changes Made

In the specification:

Paragraph beginning at page 10, line 29, has been amended as follows:

Figure 3 depicts alignment of the rat neuroligin-2 amino acid sequence and the human 33410 (SEQ ID NO:2) amino acid sequences. The location of the transmembrane domain in the rat neuroligin-2 (SEQ ID NO:5) and 33410 amino acid sequences is indicated as "TM1".

Paragraph beginning at page 10, line 32, has been amended as follows:

Figure 4 depicts alignment of the partial human KIAA1366 (Genbank Accession Number AB037787; SEQ ID NO:6) and the human 33410 amino acid sequences (SEQ ID NO:2).

Paragraph beginning at page 12, line 27, has been amended as follows:

Carboxylesterase family members are characterized by a catalytic triad of amino acids: a serine, a glutamate or aspartate and a histidine. The sequence around the active site serine is well conserved and can be used as a signature pattern. A second signature pattern is located in the N-terminal section and contains a cysteine involved in disulfide bond formation. Typical consensus patterns of carboxylesterases are F-[GR]-G-x(4)-[LIVM]-x-[LIV]-x-G-x-S-[STAG]-G (SEQ ID NO:7) (where S is the active site residue) and [ED]-D-C-L-[YT]-[LIV]-[DNS]-[LIV]-[LIVFYW]-x-[PQR] (where C is involved in a disulfide bond). 33410 proteins have a similar pattern starting at about amino acid 252 to 267 of SEQ ID NO:2 as follows:

FGGDPERITIFGSGAG.

Paragraph beginning at page 14, line 4, has been amended as follows:

As used herein, the term "carboxylesterase domain" refers to a protein domain which includes a carboxylesterase type B signature 2 domain. Preferably, the carboxylesterase type B signature 2 domain is about 5 to 20 amino acids, more preferably 8-15, most preferably 11 amino acids and includes the sequence [EDX(0,1)CLYX] (SEQ ID NO:8). Most preferably, the carboxylesterase type B signature 2 domain has the amino acid sequence: EDCLYNIYVP

located at about amino acids 139 to 149 of SEQ ID NO:2. Preferably, the carboxylesterase domain has an amino acid sequence of about 450 to about 650 amino acid residues and having a bit score for the alignment of the sequence to the carboxylesterase domain (HMM) of at least 100. Preferably, a carboxylesterase domain includes at least about 450 to about 600 amino acids, more preferably about 500 to about 575 amino acid residues, about 550 to 570, or about 559 amino acids and has a bit score for the alignment of the sequence to the carboxylesterase domain (HMM) of at least 200, preferably 300, more preferably 400 or greater. The carboxylesterase domain (HMM) has been assigned the PFAM Accession (PF00135) (<http://genome.wustl.edu/Pfam/html>). An alignment of the carboxylesterase domain (from about amino acids 42 to about 601 of SEQ ID NO:2) of human 33410 with a consensus amino acid sequence derived from a hidden Markov model (PFAM) is depicted in Figure 3.